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EPR
- (b) amino acids 2 to 127 of SEQ ID NO:2; and
 - (c) the amino acid sequence encoded by the cDNA clone contained in
ATCC Deposit No. 97856;

wherein percent identity is calculated using BESTFIT with the parameters set such that percentage of identity is calculated over the full length of the reference nucleic acid and that gaps in homology of up to 5% of the total number of nucleotides in the reference nucleic acid are allowed.

Remarks

Reconsideration of this Application is respectfully requested.

Applicants have amended claim 71 for clarity. This change is believed to introduce no new matter, and its entry is respectfully requested.

Based on the above amendment and the following remarks, Applicants respectfully request that the Examiner reconsider all outstanding objections and rejections and that they be withdrawn.

Restriction Requirement

The Examiner refused rejoinder of claim 79 with claims 16-78. The Examiner stated that

[a]s discussed . . . in M.P.E.P. 803.04, the partial waiver of the requirements of 37 CFR [sic] 1.141 is to be applied to DNA fragments comprising DNA having at least 95% homology to a single SEQ ID NO, and a combination of DNA fragments comprising a single SEQ ID NO.